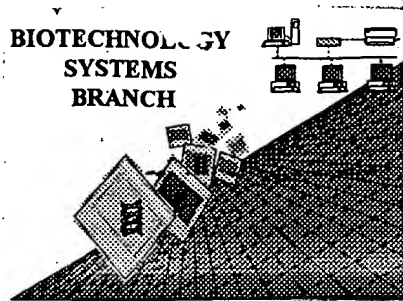


Nickol

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



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JAN 10 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: TECH CENTER 1600/2900

Application Serial Number: 09/451,739B

Source: 1642

Date Processed by STIC: 1/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/457,239B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 J Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 J Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 J Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213> Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220> Feature Sequence(s) are missing the <220> Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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JAN 10 2001

1642

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001
 TIME: 11:02:39

Input Set : A:\ES.txt
 Output Set: N:\CRF3\01022001\I451739B.raw

TECH CENTER 1600/2800

Does Not Comply
 Corrected Diskette Needed

*see item 5 on
 Enol
 Summary
 Sheet*

1 <110> APPLICANT: Jager, Dirk
 2 Scanlan, Matthew
 3 Gure, Ali
 4 Jager, Elke
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
 10 Antigens,
 11 the Antigens per se, and Uses Thereof
 13 <130> FILE REFERENCE: LUD 5615
 15 <140> CURRENT APPLICATION NUMBER: 09/451,739B
 17 <141> CURRENT FILING DATE: 1999-11-30
 19 <160> NUMBER OF SEQ ID NOS: 19

ERRORED SEQUENCES

520 <210> SEQ ID NO: 16
 521 <211> LENGTH: 513 *512 shown (next page)*
 522 <212> TYPE: PR1
 523 <213> ORGANISM: Homo sapiens
 524 <400> SEQUENCE: 16
 525 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
 526 1 5 10 15
 528 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 529 20 25 30
 531 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 532 35 40 45
 534 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
 535 50 55 60
 537 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 538 65 70 75 80
 540 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
 541 85 90 95
 543 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
 544 100 105 110
 547 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
 548 115 120 125
 550 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
 551 130 135 140
 553 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
 554 145 150 155 160
 556 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
 557 165 170 175
 559 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
 560 180 185 190

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001

TIME: 11:02:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022001\I451739B.raw

```

562 Ser Glu Ser Leu Arg Glu Thr Val Ser Glu Lys Asp Val Cys Val Pro
563      195      200      205
565 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
566      210      215      220
568 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
569 225      230      235      240
571 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 572      243 245      250 250      255 255
574 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 575      260 260      265 265      270 270
577 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
E--> 578      275      280      285
580 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
E--> 581 290      295      300      305
583 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
E--> 584      310      315      320
586 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
E--> 587      325      330      335
589 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
E--> 590      340      345      350
592 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 593      355      360      365
595 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 596 370      375      380      385
598 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 599      390      395      400
601 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
E--> 602      405      410      415
604 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
E--> 605      420      425      430
607 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
E--> 608      435      440      445
610 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
E--> 611 450      455      460      465
613 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 615      470      475      480
617 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 618      485      490      495
620 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 621      500      505      510

```

*misaligned amino
acid numbers
(see item 4 on
Error summary
sheet)*

see next page for more errors

```

<210> 1
<211> 1533
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 235
<400> 1
ggttttccac gttggacaag tgcggctcgg cggccagcgg agcgcgcccc ttcccgtgc 60
ccgctccgct cctctcttct acccagccca gtgggcgagt gggcagcggc ggccgcggcg 120
ctgggccctc tcccgcgggt gtgtgcgcgc tcgtacgcgc ggcccccggc gccagccccg 180
ccgcctgaga gggggcctgc gccgcgggcc ggggcgtgcg cccgggagcc accgncaccg 240
cggccccgcgc cctcaggcgc tggggtcccc gcggaccggg aggcggcgga cgggctcggc 300
agatgtagcc gccgggccga agcaggagcc ggcggggggg cgccgggaga gcgagggctt 360
tgcattttgc agtgctatct tttgaggggg gcggaggggt gaggaagtcg gaaagccgcg 420
ccgagtcgcc ggggacctcc ggggtgaacc atgttgagtc ctgccaacgg ggagcagctc 480
cacctgggtga actatgtgga ggactacctg gactccatcg agtccttgcc ttctgacttg 540
cagagaaatg tctcgtgat gcgggagatc gacgcgaaat accaagagat cctgaaggag 600
ctagacgagt gctacgagcg cttcagtcgc gagacagacg gggcgagcaa gcggcggtatg 660
ctgcaactgtg tgcagcgcgc gctgatccgc agccaggagc tgggcgacga gaagatccag 720
atcgtgagcc agatggtgga gctggtggag aaccgcacgc ggcaggtgga cagccacgtg 780
gagctgttcg aggcgcagca ggagctgggc gacacagcgg gcaacagcgg caaggctggc 840
gcggacaggc ccaaaggcga ggcggcagcg caggctgaca agcccaacag caagcgctca 900
cggcggcagc gcaacaacga gaaccgtgag aacgcgtcca gcaaccacga ccacgacgac 960
ggcgccctcg gcacacccaa ggagaagaag gccaagacct ccaagaagaa gaagcgctcc 1020
aaggccaagg cggagcgaga ggcgtcccct gccgacctcc ccatcgacct caacgaacct 1080
acgtactgtc tgtgcaacca ggtctcctat ggggagatga tcggctgcga caacgacgag 1140
tgccccatcg agtgggtcca cttctcgtgc gtggggctca atcataaacc caagggcaag 1200
tggtactgtc ccaagtgccg gggggagaac gagaagacca tggacaaagc cctggagaaa 1260
tccaaaaaag agagggctta caacaggtag tttgtggaca ggcgcctggt gtgaggagga 1320
caaaataaac cgtgtattta ttacattgct gcctttgttg aggtgcaagg agtgtaaaat 1380
gtatatTTTT aaagaatggt agaaaaggaa ccattccttt catagggatg gcagtgattc 1440
tgtttgcctt ttgttttcat tggtagacgt gtaacaagaa agtggtctgt ggatcagcat 1500
tttagaaact acaaatatag gtttgattca aca 1533

```

→ see
item 10
on Encl
Summary Sheet

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001
TIME: 11:02:40

Input Set : A:\ES.txt
Output Set : N:\CRF3\01022001\I451739B.raw

L:26 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:36 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:367 M:283 W: Missing Blank Line separator, <400> field identifier
L:390 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:390 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:390 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:407 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:283 W: Missing Blank Line separator, <400> field identifier
L:423 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:450 M:283 W: Missing Blank Line separator, <400> field identifier
L:505 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:505 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:515 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:515 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:517 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:524 M:283 W: Missing Blank Line separator, <400> field identifier
L:572 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:621 M:252 E: No. of Seq. differs, <211>LENGTH:Input:513 Found:512 SEQ:16
L:628 M:283 W: Missing Blank Line separator, <400> field identifier
L:636 M:283 W: Missing Blank Line separator, <400> field identifier
L:644 M:283 W: Missing Blank Line separator, <400> field identifier